

QIPE

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/731,657

DATE: 11/29/2001
TIME: 15:35:50

Input Set : A:\09731657.raw.txt
Output Set: N:\CRF3\11292001\I731657.raw

SEQUENCE LISTING

ENTERED

3 (1) GENERAL INFORMATION:
5 (i) APPLICANT: OSTERHOFF, CAROLINE
6 IVELL, RICHARD
8 (ii) TITLE OF INVENTION: EPIDIDYMIS-SPECIFIC RECEPTOR PROTEIN
10 (iii) NUMBER OF SEQUENCES: 11
12 (iv) CORRESPONDENCE ADDRESS:
13 (A) ADDRESSEE: NIXON & VANDERHYE P.C.
14 (B) STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
15 (C) CITY: ARLINGTON
16 (D) STATE: VA
17 (E) COUNTRY: USA
18 (F) ZIP: 22201
20 (v) COMPUTER READABLE FORM:
21 (A) MEDIUM TYPE: Floppy disk
22 (B) COMPUTER: IBM PC compatible
23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30
26 (vi) CURRENT APPLICATION DATA:
C--> 27 (A) APPLICATION NUMBER: US/09/731,657
C--> 28 (B) FILING DATE: 12-Mar-2001
29 (C) CLASSIFICATION:
31 (vii) PRIOR APPLICATION DATA:
32 (A) APPLICATION NUMBER: US/09/041,745
33 (B) FILING DATE:
35 (viii) ATTORNEY/AGENT INFORMATION:
36 (A) NAME: SADOFF, B.J.
37 (B) REGISTRATION NUMBER: 36,663
38 (C) REFERENCE/DOCKET NUMBER: 35-125
40 (ix) TELECOMMUNICATION INFORMATION:
41 (A) TELEPHONE: 703-816-4000
42 (B) TELEFAX: 703-816-4100
45 (2) INFORMATION FOR SEQ ID NO: 1:
47 (i) SEQUENCE CHARACTERISTICS:
48 (A) LENGTH: 4665 base pairs
49 (B) TYPE: nucleic acid
50 (C) STRANDEDNESS: single
51 (D) TOPOLOGY: linear
53 (ii) MOLECULE TYPE: cDNA
55 (ix) FEATURE:
56 (A) NAME/KEY: CDS
57 (B) LOCATION: 1..3114
59 (ix) FEATURE:
60 (A) NAME/KEY: 3'UTR
61 (B) LOCATION: 3115..4665
63 (ix) FEATURE:
64 (A) NAME/KEY: polyA-site

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65	(B) LOCATION: 4647..4652			
67	(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:			
70	AGC	CAG	CCC GAG GAC GCG AGC GGC AGG TGT GCA CAG AGG TTC TCC ACT	48
71	Ser	Gln	Pro Glu Asp Ala Ser Gly Arg Cys Ala Gln Arg Phe Ser Thr	
72	1	5	10	15
74	TTG	TTT	TCT GAA CTC GCG GTC AGG ATG GTT TTC TCT GTC AGG CAG TGT	96
75	Leu	Phe	Ser Glu Leu Ala Val Arg Met Val Phe Ser Val Arg Gln Cys	
76	20	25	30	
78	GGC	CAT	GTT GGC AGA ACT GAA GAA GTT TTA CTG ACG TTC AAG ATA TTC	144
79	Gly	His	Val Gly Arg Thr Glu Glu Val Leu Leu Thr Phe Lys Ile Phe	
80	35	40	45	
82	CTT	GTC	ATC ATT TGT CTT CAT GTC GTT CTG GTA ACA TCC CTG GAA GAA	192
83	Leu	Val	Ile Cys Leu His Val Val Leu Val Thr Ser Leu Glu Glu	
84	50	55	60	
86	GAT	ACT	GAT AAT TCC AGT TTG TCA CCA CCA CCT GCT AAA TTA TCT GTT	240
87	Asp	Thr	Asp Asn Ser Ser Leu Ser Pro Pro Pro Ala Lys Leu Ser Val	
88	65	70	75	80
90	GTC	AGT	TTT GCC CCC TCC TCC AAT GAG GTT GAA ACA ACA AGC CTC AAT	288
91	Val	Ser	Phe Ala Pro Ser Ser Asn Glu Val Glu Thr Thr Ser Leu Asn	
92	85	90	95	
94	GAT	GTT	ACT TTA AGC TTA CTC CCT TCA AAC GAA ACA GAA AAA ACT AAA	336
95	Asp	Val	Thr Leu Ser Leu Leu Pro Ser Asn Glu Thr Glu Lys Thr Lys	
96	100	105	110	
98	ATC	ACT	ATA GTA AAA ACC TTC AAT GCT TCA GGC GTC AAA CCC CAG AGA	384
99	Ile	Thr	Ile Val Lys Thr Phe Asn Ala Ser Gly Val Lys Pro Gln Arg	
100	115	120	125	
102	AAT	ATC	TGC AAT TTG TCA TCT ATT TGC AAT GAC TCA GCA TTT TTT AGA	432
103	Asn	Ile	Cys Asn Leu Ser Ser Ile Cys Asn Asp Ser Ala Phe Phe Arg	
104	130	135	140	
106	GGT	GAG	ATC ATG TTT CAA TAT GAT AAA GAA AGC ACT GTT CCC CAG AAT	480
107	Gly	Glu	Ile Met Phe Gln Tyr Asp Lys Glu Ser Thr Val Pro Gln Asn	
108	145	150	155	160
110	CAA	CAT	ATA ACG AAT GGC ACC TTA ACT GGA GTC CTG TCT CTA AGT GAA	528
111	Gln	His	Ile Thr Asn Gly Thr Leu Thr Gly Val Leu Ser Leu Ser Glu	
112	165	170	175	
114	TTA	AAA	CGC TCA GAG CTC AAC AAA ACC CTG CAA ACC CTA AGT GAG ACT	576
115	Leu	Lys	Arg Ser Glu Leu Asn Lys Thr Leu Gln Thr Leu Ser Glu Thr	
116	180	185	190	
118	TAC	TTT	ATA ATG TGT GCT ACA GCA GAG GCC CAA AGC ACA TTA AAT TGT	624
119	Tyr	Phe	Ile Met Cys Ala Thr Ala Glu Ala Gln Ser Thr Leu Asn Cys	
120	195	200	205	
122	ACA	TTC	ACA ATA AAA CTG AAT ACA ATG AAT GCA TGT GCT GCA ATA	672
123	Thr	Phe	Thr Ile Lys Leu Asn Asn Thr Met Asn Ala Cys Ala Ala Ile	
124	210	215	220	
126	GCC	GCT	TTG GAA AGA GTA AAG ATT CGA CCA ATG GAA CAC TGC TGC TGT	720
127	Ala	Ala	Leu Glu Arg Val Lys Ile Arg Pro Met Glu His Cys Cys Cys	
128	225	230	235	240
130	TCT	GTC	AGG ATA CCC TGC CCT TCC CCA GAA GAG TTG GGA AAG CTT	768
131	Ser	Val	Arg Ile Pro Cys Pro Ser Ser Pro Glu Glu Leu Gly Lys Leu	

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132	245	250	255	
134	CAG TGT GAC CTG CAG GAT CCC ATT GTC TGT CTT GCT GAC CAT CCA CGT			816
135	Gln Cys Asp Leu Gln Asp Pro Ile Val Cys Leu Ala Asp His Pro Arg			
136	260	265	270	
138	GGC CCA CCA TTT TCT TCC AGC CAA TCC ATC CCA GTG GTG CCT CGG GCC			864
139	Gly Pro Pro Phe Ser Ser Ser Gln Ser Ile Pro Val Val Pro Arg Ala			
140	275	280	285	
142	ACT GTG CTT TCC CAG GTC CCC AAA GCT ACC TCT TTT GCT GAG CCT CCA			912
143	Thr Val Leu Ser Gln Val Pro Lys Ala Thr Ser Phe Ala Glu Pro Pro			
144	290	295	300	
146	GAT TAT TCA CCT GTG ACC CAC AAT GTT CCC TCT CCA ATA GGG GAG ATT			960
147	Asp Tyr Ser Pro Val Thr His Asn Val Pro Ser Pro Ile Gly Glu Ile			
148	305	310	315	320
150	CAA CCC CTT TCA CCC CAG CCT TCA GCT CCC ATA GCT TCC AGC CCT GCC			1008
151	Gln Pro Leu Ser Pro Gln Pro Ser Ala Pro Ile Ala Ser Ser Pro Ala			
152	325	330	335	
154	ATT GAC ATG CCC CCA CAG TCT GAA ACG ATC TCT TCC CCT ATG CCC CAA			1056
155	Ile Asp Met Pro Pro Gln Ser Glu Thr Ile Ser Ser Pro Met Pro Gln			
156	340	345	350	
158	ACC CAT GTC TCC GGC ACC CCA CCT CCT GTG AAA GCC TCA TTT TCC TCT			1104
159	Thr His Val Ser Gly Thr Pro Pro Val Lys Ala Ser Phe Ser Ser			
160	355	360	365	
162	CCC ACC GTG TCT GCC CCT GCG AAT GTC AAC ACT ACC AGC GCA CCT CCT			1152
163	Pro Thr Val Ser Ala Pro Ala Asn Val Asn Thr Thr Ser Ala Pro Pro			
164	370	375	380	
166	GTC CAG ACA GAC ATC GTC AAC ACC AGC AGT ATT TCT GAT CTT GAG AAC			1200
167	Val Gln Thr Asp Ile Val Asn Thr Ser Ser Ile Ser Asp Leu Glu Asn			
168	385	390	395	400
170	CAA GTG TTG CAG ATG GAG AAG GCT CTG TCC TTG GGC AGC CTG GAG CCT			1248
171	Gln Val Leu Gln Met Glu Lys Ala Leu Ser Leu Gly Ser Leu Glu Pro			
172	405	410	415	
174	AAC CTC GCA GGA GAA ATG ATC AAC CAA GTC AGC AGA CTC CTT CAT TCC			1296
175	Asn Leu Ala Gly Glu Met Ile Asn Gln Val Ser Arg Leu Leu His Ser			
176	420	425	430	
178	CCG CCT GAC ATG CTG GCC CCT CTG GCT CAA AGA TTG CTG AAA GTA GTG			1344
179	Pro Pro Asp Met Leu Ala Pro Leu Ala Gln Arg Leu Leu Lys Val Val			
180	435	440	445	
182	GAT GAC ATT GGC CTA CAG CTG AAC TTT TCA AAC ACG ACT ATA AGT CTA			1392
183	Asp Asp Ile Gly Leu Gln Leu Asn Phe Ser Asn Thr Thr Ile Ser Leu			
184	450	455	460	
186	ACC TCC CCT TCT TTG GCT CTG GCT GTG ATC AGA GTG AAT GCC AGT AGT			1440
187	Thr Ser Pro Ser Leu Ala Leu Ala Val Ile Arg Val Asn Ala Ser Ser			
188	465	470	475	480
190	TTC AAC ACA ACT ACC TTT GTG GCC CAA GAC CCT GCA AAT CTT CAG GTT			1488
191	Phe Asn Thr Thr Phe Val Ala Gln Asp Pro Ala Asn Leu Gln Val			
192	485	490	495	
194	TCT CTG GAA ACC CAA GCT CCT GAG AAC AGT ATT GGC ACA ATT ACT CTT			1536
195	Ser Leu Glu Thr Gln Ala Pro Glu Asn Ser Ile Gly Thr Ile Thr Leu			
196	500	505	510	

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198 CCT TCA TCG CTG ATG AAT AAT TTA CCA GCT CAT GAC ATG GAG CTA GCT	1584
199 Pro Ser Ser Leu Met Asn Asn Leu Pro Ala His Asp Met Glu Leu Ala	
200 515 520 525	
202 TCC AGG GTT CAG TTC AAT TTT TTT GAA ACA CCT GCT TTG TTT CAG GAT	1632
203 Ser Arg Val Gln Phe Asn Phe Phe Glu Thr Pro Ala Leu Phe Gln Asp	
204 530 535 540	
206 CCT TCC CTG GAG AAC CTC TCT CTG ATC AGC TAC GTC ATA TCA TCG AGT	1680
207 Pro Ser Leu Glu Asn Leu Ser Leu Ile Ser Tyr Val Ile Ser Ser Ser	
208 545 550 555 560	
210 GTT GCA AAC CTG ACC GTC AGG AAC TTG ACA AGA AAC GTG ACA GTC ACA	1728
211 Val Ala Asn Leu Thr Val Arg Asn Leu Thr Arg Asn Val Thr Val Thr	
212 565 570 575	
214 TTA AAG CAC ATC AAC CCG AGC CAG GAT GAG TTA ACA GTG AGA TGT GTA	1776
215 Leu Lys His Ile Asn Pro Ser Gln Asp Glu Leu Thr Val Arg Cys Val	
216 580 585 590	
218 TTT TGG GAC TTG GGC AGA AAT GGT GGC AGA GGA GGC TGG TCA GAC AAT	1824
219 Phe Trp Asp Leu Gly Arg Asn Gly Gly Arg Gly Gly Trp Ser Asp Asn	
220 595 600 605	
222 GGC TGC TCT GTC AAA GAC AGG AGA TTG AAT GAA ACC ATC TGT ACC TGT	1872
223 Gly Cys Ser Val Lys Asp Arg Arg Leu Asn Glu Thr Ile Cys Thr Cys	
224 610 615 620	
226 AGC CAT CTA ACA AGC TTC GGC GTT CTG CTG GAC CTA TCT AGG ACA TCT	1920
227 Ser His Leu Thr Ser Phe Gly Val Leu Leu Asp Leu Ser Arg Thr Ser	
228 625 630 635 640	
230 GTG CTG CCT GCT CAA ATG ATG GCT CTG ACG TTC ATT ACA TAT ATT GGT	1968
231 Val Leu Pro Ala Gln Met Met Ala Leu Thr Phe Ile Thr Tyr Ile Gly	
232 645 650 655	
234 TGT GGG CTT TCA TCA ATT TTT CTG TCA GTG ACT CTT GTA ACC TAC ATA	2016
235 Cys Gly Leu Ser Ser Ile Phe Leu Ser Val Thr Leu Val Thr Tyr Ile	
236 660 665 670	
238 GCT TTT GAA AAG ATC CGG AGG GAT TAC CCT TCC AAA ATC CTC ATC CAG	2064
239 Ala Phe Glu Lys Ile Arg Arg Asp Tyr Pro Ser Lys Ile Leu Ile Gln	
240 675 680 685	
242 CTG TGT GCT CTG CTT CTG AAC CTG GTC TTC CTC CTG GAC TCG	2112
243 Leu Cys Ala Ala Leu Leu Leu Leu Asn Leu Val Phe Leu Leu Asp Ser	
244 690 695 700	
246 TGG ATT GCT CTG TAT AAG ATG CAA GGC CTC TGC ATC TCA GTG GCT GTA	2160
247 Trp Ile Ala Leu Tyr Lys Met Gln Gly Leu Cys Ile Ser Val Ala Val	
248 705 710 715 720	
250 TTT CTT CAT TAT TTT CTC TTG GTC TCA TTC ACA TGG ATG GGC CTA GAA	2208
251 Phe Leu His Tyr Phe Leu Leu Val Ser Phe Thr Trp Met Gly Leu Glu	
252 725 730 735	
254 GCA TTC CAT ATG TAC CTG GCC CTT GTC AAA GTA TTT AAT ACT TAC ATC	2256
255 Ala Phe His Met Tyr Leu Ala Leu Val Lys Val Phe Asn Thr Tyr Ile	
256 740 745 750	
258 CGA AAA TAC ATC CTT AAA TTC TGC ATT GTC GGT TGG GGG GTA CCA GCT	2304
259 Arg Lys Tyr Ile Leu Lys Phe Cys Ile Val Gly Trp Gly Val Pro Ala	
260 755 760 765	
262 GTG GTT GTG ACC ATC ATC CTG ACT ATA TCC CCA GAT AAC TAT GGG CTT	2352

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263	Val	Val	Val	Thr	Ile	Ile	Leu	Thr	Ile	Ser	Pro	Asp	Asn	Tyr	Gly	Leu	
264	770				775				780								
266	GGA	TCC	TAT	GGG	AAA	TTC	CCC	AAT	GGT	TCA	CCG	GAT	GAC	TTC	TGC	TGG	2400
267	Gly	Ser	Tyr	Gly	Lys	Phe	Pro	Asn	Gly	Ser	Pro	Asp	Asp	Phe	Cys	Trp	
268	785				790				795							800	
270	ATC	AAC	AAC	AAT	GCA	GTA	TTC	TAC	ATT	ACG	GTG	GTG	GGA	TAT	TTC	TGT	2448
271	Ile	Asn	Asn	Asn	Ala	Val	Phe	Tyr	Ile	Thr	Val	Val	Gly	Tyr	Phe	Cys	
272					805				810							815	
274	GTG	ATA	TTT	TTG	CTG	AAC	GTC	AGC	ATG	TTC	ATT	GTG	GTC	CTG	GTT	CAG	2496
275	Val	Ile	Phe	Leu	Leu	Asn	Val	Ser	Met	Phe	Ile	Val	Val	Leu	Val	Gln	
276					820				825							830	
278	CTC	TGT	CGA	ATT	AAA	AAG	AAG	AAG	CAA	CTG	GGA	GCC	CAG	CGA	AAA	ACC	2544
279	Leu	Cys	Arg	Ile	Lys	Lys	Lys	Gln	Leu	Gly	Ala	Gln	Arg	Lys	Thr		
280					835				840							845	
282	AGT	ATT	CAA	GAC	CTC	AGG	AGT	ATC	GCT	GGC	CTT	ACA	TTT	TTA	CTG	GGA	2592
283	Ser	Ile	Gln	Asp	Leu	Arg	Ser	Ile	Ala	Gly	Leu	Thr	Phe	Leu	Leu	Gly	
284					850				855							860	
286	ATA	ACT	TGG	GGC	TTT	GCC	TTC	TTT	GCC	TGG	GGA	CCA	GTT	AAC	GTG	ACC	2640
287	Ile	Thr	Trp	Gly	Ala	Phe	Phe	Ala	Trp	Gly	Pro	Val	Asn	Val	Thr		
288					865				870							880	
290	TTC	ATG	TAT	CTG	TTT	GCC	ATC	TTT	AAT	ACC	TTA	CAA	GGA	TTT	TTC	ATA	2688
291	Phe	Met	Tyr	Leu	Phe	Ala	Ile	Phe	Asn	Thr	Leu	Gln	Gly	Phe	Phe	Ile	
292					885				890							895	
294	TTC	ATC	TTT	TAC	TGT	GTG	GCC	AAA	GAA	AAT	GTC	AGG	AAG	CAA	TGG	AGG	2736
295	Phe	Ile	Phe	Tyr	Cys	Val	Ala	Lys	Glu	Asn	Val	Arg	Lys	Gln	Trp	Arg	
296					900				905							910	
298	CGG	TAT	CTT	TGT	TGT	GGG	AAG	TTA	CGG	CTG	GCT	GAA	AAT	TCT	GAC	TGG	2784
299	Arg	Tyr	Leu	Cys	Cys	Gly	Lys	Leu	Arg	Leu	Ala	Glu	Asn	Ser	Asp	Trp	
300					915				920							925	
302	AGT	AAA	ACT	GCT	ACT	AAT	GGT	TTA	AAG	AAG	CAG	ACT	GTA	AAC	CAA	GGA	2832
303	Ser	Lys	Thr	Ala	Thr	Asn	Gly	Leu	Lys	Lys	Gln	Thr	Val	Asn	Gln	Gly	
304					930				935							940	
306	GTG	TCC	AGC	TCT	TCA	AAT	TCC	TTA	CAG	TCA	AGC	AGT	AAC	TCC	ACT	AAC	2880
307	Val	Ser	Ser	Ser	Ser	Asn	Ser	Leu	Gln	Ser	Ser	Ser	Asn	Ser	Thr	Asn	
308					945				950							960	
310	TCC	ACC	ACA	CTG	CTA	GTG	AAT	AAT	GAT	TGC	TCA	GTA	CAC	GCA	AGC	GGG	2928
311	Ser	Thr	Thr	Leu	Leu	Val	Asn	Asn	Asp	Cys	Ser	Val	His	Ala	Ser	Gly	
312					965				970							975	
314	AAT	GGA	AAT	GCT	TCT	ACA	GAG	AGG	AAT	GGG	GTC	TCT	TTT	AGT	GTT	CAG	2976
315	Asn	Gly	Asn	Ala	Ser	Thr	Glu	Arg	Asn	Gly	Val	Ser	Phe	Ser	Val	Gln	
316					980				985							990	
318	AAT	GGA	GAT	GTG	TGC	CTT	CAC	GAT	TTC	ACT	GGA	AAA	CAG	CAC	ATG	TTT	3024
319	Asn	Gly	Asp	Val	Cys	Leu	His	Asp	Phe	Thr	Gly	Lys	Gln	His	Met	Phe	
320					995				1000							1005	
322	AAC	GAG	AAG	GAT	TCC	TGC	AAT	GGG	AAA	GGC	CGT	ATG	GCT	CTC	AGA		3072
323	Asn	Glu	Lys	Glu	Asp	Ser	Cys	Asn	Gly	Lys	Gly	Arg	Met	Ala	Leu	Arg	
324					1010				1015							1020	
326	AGG	ACT	TCA	AAG	CGG	GGG	AGC	TTA	CAC	TTT	ATT	GAG	CAA	ATG			3114
327	Arg	Thr	Ser	Lys	Arg	Gly	Ser	Leu	His	Phe	Ile	Glu	Gln	Met			

VERIFICATION SUMMARY

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L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]

L:751 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:11